Table S1. Number of shared islands between paired comparisons.

Class of shared islands[a]	Species pairs	*ALX1* haplogroup	*HMGA2* haplogroup	No. of shared windows	Annotation	*P* value[b]
(A) Between ground-ground and tree-tree finch pairs	*G.magnirostris_G* vs. *G.propinqua_G*	different	same	0		1.000
	C.pauper_F vs. *C.psittacula_P*	same	different			
	G.magnirostris_G vs. *G.acutirostris_G*	different	different	8	7 windows located in *HMGA2* locus	0.001
	C.pauper_F vs. *C.psittacula_P*	same	different			
	G.magnirostris_G vs. *G.magnirostris_M*	same	same	3		0.009
	C.pauper_F vs. *C.psittacula_P*	same	different			
(B) Between ground-tree and ground-tree finch pairs	*G.fuliginosa_S* vs. *C.parvulus_Z*	same	same	17		0
	G.magnirostris_M vs. *C.parvulus_Z*	different	different			
	G.fuliginosa_S vs. *C.parvulus_Z*	same	same	2		0.031
	G.magnirostris_M vs. *C.pallidus_Z*	different	same			
(C) Between more distantly related pairs	*P.crassirostris_Z* vs. *C.parvulus_Z*	same	different	6	3 windows located in *HMGA2* locus	0
	P.inornata_C vs.*G.magnirostris_M*	different	different			
	G.magnirostris_G vs. *G.propinqua_G*	different	same	9	2 windows located in *HMGA2* locus and 3 in *ALX1* locus	0
	P.inornata_C vs.*G.magnirostris_M*	different	different			

[a] Class A and B identified the shared islands between ground- and tree- finch pairs. Pairwise comparisons in class A represent species pairs from independent branches in phylogeny while class B and C involve shared lineages.

[b] Significance is estimated with randomization test.